**Amendments to the Specification**

Please replace the paragraph beginning at page 1, line 13, with the following rewritten paragraph:

Methods utilizing mass spectrometry for the analysis of a target polypeptide have been taught wherein the polypeptide is first solubilized in an appropriate solution or reagent system. The type of solution or reagent system, e.g., comprising an organic or inorganic solvent, will depend on the properties of the polypeptide and the type of mass spectrometry performed and are well-known in the art (see, e.g. Vorm et al. (1994) Anal. Chem. 66:3281 (for MALDI) and Valaskovic et al. (1995) Anal. Chem. 67:3802 (for ESI)). Mass spectrometry of peptides is further disclosed, e.g. in WO 93/24834 by Chait et al.

Please replace the paragraph beginning at page 4, line 19, with the following rewritten paragraph:

~~PCT/EP/04396~~ PCT/EP97/04396 (WO 98/07036) teaches a process for determining the status of an organism by peptide measurement. The reference teaches the measurement of peptides in a sample of the organism which contains both high and low molecular weight peptides and acts as an indicator of the organism's status. The reference concentrates on the measurement of low molecular weight peptides , i.e. below 30,000 Daltons, whose distribution serves as

a representative cross-section of defined controls. Contrary to the methodology of the instant invention, the '396 patent strives to determine the status of a healthy organism, i.e. a "normal" and then use this as a reference to differentiate disease states. The present inventors do not attempt to develop a reference "normal", but rather strive to specify particular markers which are evidentiary of at least one specific disease state, whereby the presence of said marker serves as a positive indicator of disease. This leads to a simple method of analysis which can easily be performed by an untrained individual, since there is a positive correlation of data. On the contrary, the '396 patent requires a complicated analysis by a highly trained individual to determine disease state versus the perception of non-disease or normal physiology.

Please replace the paragraph beginning at page 6, line 5, with the following rewritten paragraph:

As used herein, "analyte" refers to any atom and/or molecule; including their complexes and fragment ions. In the case of biological molecules/macromolecules or "biopolymers", such analytes include but are not limited to: proteins, peptides, DNA, RNA, carbohydrates, steroids, and lipids. Note that most important biomolecules under investigation for their involvement in the

structure or regulation of life processes are quite large (typically several thousand times larger than $H_2O$).

Please replace the paragraph beginning at page 19, line 2, with the following rewritten paragraph:

Figure 1 is a representation of derived data which characterizes a disease specific marker having a particular sequence, SEQ ID NO:1, useful in evidencing and categorizing at least one particular disease state; and

Figure 2 is the characteristic profile derived via SELDI/TOF MS of the disease specific marker ~~of figure 1~~ , SEQ ID NO:1.

Please replace the paragraph beginning at page 21, line 7, with the following rewritten paragraph:

Spotting was then performed, for example on a Gold Chip in the following manner:

1. spot 2µl of sample onto each [[spot]] chip
2. let sample partially dry
3. spot 1µl of [[matrx]] matrix, and let air dry.

Please replace the paragraph beginning at page 21, line 12, with the following rewritten paragraph:

**HiQ Anion Exchange Mini Column Protocol**

1) Dilute sera in sample/running buffer;
2) Add HiQ resin to column and remove any air bubbles;
3) Add ultrafiltered (UF) [[Uf]] water to aid in column packing;
4) Add sample/running buffer to equilibrate column;
5) Add diluted sera;
6) Collect all the flow-through fraction in ~~Eppendorf~~ EPPENDORF tubes until level is at resin;
7) Add sample/running buffer to wash column; and
8) Add ~~elusion~~ elution buffer and collect ~~elusion~~ elution in ~~Eppendorf~~ EPPENDORF tubes.

Please replace the paragraph beginning at page 22, line 2, with the following rewritten paragraph:

Sample/Running buffers: including but not limited to Bicine buffers of various molarities, pH's, NaCl content, ~~Bis-Tris~~ BIS-TRIS buffers of various molarities, pH's, NaCl content, Diethanolamine of various molarities, pH's, NaCl content, Diethylamine of various molarities, pH's, NaCl content, Imidazole of various molarities, pH's, NaCl content, Tricine of various

molarities, pH's, NaCl content, Triethanolamine of various molarities, pH's, NaCl content, [[Tris]] TRIS of various molarities, pH's, NaCl content.

Please replace the paragraph beginning at page 22, line 19, with the following rewritten paragraph:

**Chelating [Sepharose] SEPHAROSE Mini Column**

1. Dilute Sera in Sample/Running buffer;
2. Add Chelating [Sepharose] SEPHAROSE slurry to column and allow column to pack;
3. Add [[UF]] ultrafiltered (UF) water to the column to aid in packing;
4. Add Charging Buffer once water is at the level of the resin surface;
5. Add UF water to wash through non bound metal ions once charge buffer washes through;
6. Add running buffer to equilibrate column for sample loading;
7. Add diluted serum sample;
8. Add running buffer to wash unbound protein;
9. Add elution buffer and collect elution fractions for analysis; and
10. Acidify each elution fraction.

Please replace the paragraph beginning at page 24, line 1, with the following rewritten paragraph:

**HiS Cation Exchange Mini Column Protocol**

1) Dilute sera in sample/running buffer;
2) Add HiS resin to column and remove any air bubbles;
3) Add ultrafiltered (UF) [[Uf]] water to aid in column packing;
4) Add sample/running buffer to equilibrate column for sample loading;
5) Add diluted sera to column;
6) Collect all flow through fractions in ~~Eppendorf~~ EPPENDORF tubes until level is at resin[[.]] ;
7) Add sample/running buffer to wash column[[.]] ;and
8) Add ~~elusion~~ elution buffer and collect ~~elusion~~ elution in ~~Eppendorf~~ EPPENDORF tubes.

Please replace the paragraph beginning at page 24, line 15, with the following rewritten paragraph:

Sample/Running buffers: including but not limited to Bicine buffers of various molarities, pH's, NaCl content, ~~Bis-Tris~~ BIS-TRIS buffers of various molarities, pH's, NaCl content, Diethanolamine of various molarities, pH's, NaCl content,

Diethylamine of various molarities, pH's, NaCl content, Imidazole of various molarities, pH's, NaCl content, Tricine of various molarities, pH's, NaCl content, Triethanolamine of various molarities, pH's, NaCl content, [[Tris]] TRIS of various molarities, pH's, NaCl content.

Please replace the paragraph beginning at page 27, line 6, with the following rewritten paragraph:

For example, Serum (20ml) was (diluted 5-fold with phosphate buffered saline) concentrated by centrifugation through a YM3 MICRON spin filter ~~(Amicon)~~ (AMICON) for 20 min at 10,000 RPM at 4°C in a Beckman MICROCENTRIfuge R model bench top centrifuge. The filtrate was discarded and the retained solution, which contained the two peptides of interest, was analyzed further by tandem mass spectrometry to deduce their amino acid sequences. Tandem mass spectrometry was performed at the University of Manitoba's (Winnipeg, Manitoba, Canada) mass spectrometry laboratory using the procedures that are well known to practitioners of the art.

Please replace the paragraph beginning at page 27, line 17, with the following rewritten paragraph:

As a result of these procedures, the disease specific marker identified by the sequence ~~ITHRIHWESASLL~~ SEQ ID NO:1 was found.

This marker is characterized as a C3f fragment from the complement system having a molecular weight of about 1562 daltons. The characteristic profile of the marker is set forth in Figure 2. As easily deduced from the data set forth in Figure 1, this marker is indicative of an individual suffering from myocardial infarction or congestive heart failure.

Please replace the paragraph beginning at page 28, line 11, with the following rewritten paragraph:

The specific disease markers which are analyzed according to the method of the invention are released into the circulation and may be present in the blood or in any blood product, for example plasma, serum, cytolyzed blood, e.g. by treatment with hypotonic buffer or detergents and dilutions and preparations thereof, and other body fluids, e.g. [[CSF]] cerebrospinal fluid (CSF), saliva, urine, lymph, and the like. The presence of each marker is determined using antibodies specific for each of the markers and detecting specific binding of each antibody to its respective marker. Any suitable direct or indirect assay method may be used to determine the level of each of the specific markers measured according to the invention. The assays may be competitive assays, sandwich assays, and the label may be selected from the group of well-known labels such as radioimmunoassay, fluorescent or

chemiluminescence immunoassay, or immunoPCR technology. Extensive discussion of the known immunoassay techniques is not required here since these are known to those of ~~skilled~~ skill in the art. See Takahashi et al. (Clin Chem 1999; 45(8): 1307) for S100B assay.

Please replace the paragraph beginning at page 36, line 2, with the following re-written paragraph:

The instant invention involves the use of a combination of preparatory steps in conjunction with mass spectroscopy and time-of-flight detection procedures to maximize the diversity of biopolymers which are verifiable within a particular sample. The cohort of biopolymers verified within such a sample is then viewed with reference to their ability to evidence at least one particular disease state; thereby enabling a diagnostician to gain the ability to characterize either the presence or absence of [[said]] at least one disease state relative to recognition of the presence and/or the absence of [[said]] the biopolymer.